

Figure 1

M	G	T	P	A	Q	I	L	G	F
ATG	GGG	GCC	CCT	GCT	CAG	ATT	CTT	GGG	TTC
L	L	L	L	F	P	G	T	R	C
TTG	TTG	CTC	TTG	TTT	CCA	GGT	ACC	AGA	TGT
(leader, -20-1)									

D	I	Q	M	T	Q	S	P	S	S
GAC	ATC	CAG	ATG	ACC	CAG	TCT	CCA	TCC	TCC
L	S	A	S	L	G	Q	R	V	S
TTA	TCT	GCC	TCT	CTG	CGA	CAA	AGA	GTC	AGT
L	T	C							
CTC	ACT	TGT	(fr.1, 1-23)						

R	A	S	Q	D	I	G	I	N	L
CGG	GCA	AGT	CAG	GAC	ATT	GGT	ATT	AAC	TTA
H									
CAT	(cdr1, 24-34)								

T	L	Q	Q	E	P	D	G	T	I
TGG	CTT	CAG	CAG	GAA	CCA	GAT	GGA	ACT	ATT
K	R	L	I	Y					
AAA	CGC	CTG	ATC	TAC	(fr2., 35-49)				

A	T	S	S	L	G	S			
GCC	ACA	TCC	AGT	TTA	GGT	TCT			
							(cdr2, 50-56)		

G	V	P	K	R	F	S	G	S	R
GGT	GTC	CCC	AAA	AGG	TTC	AGT	GGC	AGT	AGG
S	G	S	D	Y	S	L	T	I	S
TCT	GGG	TCA	GAT	TAT	TCT	CTC	ACC	ATC	AGC
S	L	E	S	G	D	F	V	A	Y
AGC	CTT	GAG	TCT	GAA	GAT	TTT	GTA	GCC	TAT
Y	C								
TAC	TGT	(fr3, 57-88)							

L	Q	Y	A	S	S	P	Y	T	
CTA	CAA	TAT	GCT	AGT	TCT	CCG	TAC	ACG	
(cdr3, 89-97)									

F	G	G	G	T	K	L	E	I	K
TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAA	ATA	AAA
(fr4, 98-107)									

R	A	D	A	A	P	T	V	S	I
CGG	GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC
F	P	P	S	S	K	L	G		
TTC	CCA	CCA	TCC	AGT	AAG	CTT	GGG		

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Figure 2

M E C S W V F L F L L S I T T G V
ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT GTC
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Ser Ile Thr Thr Gly Val

H S
CAC TCC
His Ser (leader)

Q A Y L Q Q S G A E L V R S
CAG GCT TAT CTA CAG CAG TCT GGG CCT GAG CTG GTG AGG TCT
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser

G A S V K M S C K A S G Y T L T
GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG ACC
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr
(1-30, Fr. #1)

S Y N M H
AGT TAC AAT ATG CAC
Ser Tyr Asn Met His (31-35, CDR 1)

W V K Q T P G Q G L E W I G
TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG GAA TGG ATT GGA
Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly

(36-49, Fr. #2)

N I F P G N G D T Y Y N Q K F K G
AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT CAG AAG TTT AAG GGC
Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn Gln Lys Phe Lys Gly
(50-66, CDR 2)

K A S L T A D T S S S T A Y M Q
AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC ACA GCC TAC ATG CAG
Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Thr Ala Tyr Met Gln

I S S L T S E D S A V Y F C A R
ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC TAT TTC TGT GCA AGA
Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg

(67-98, Fr. #3)

G N W E G A L D Y
GGG AAC TGG CAG GGT GCT CTG GAC TAC
Gly Asn Trp Glu Gly Ala Leu Asp Tyr

(99-107, CDR 3)

W G Q G T S V T V S S
TGG GGT CAA CGA ACC TCA GTC ACC GTC TCC TCA
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

(108-118, Fr. #4)

A K T T P P V Y P L V P G S L
GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
Ala Lys Thr Thr Pro Pro Val Tyr Pro Leu Val Pro Gly Ser Leu

(constant region)

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Figure 3A

DIQMTQSPSSLSASLGQRVSLTC — Framework #1, 1–23

RASQDIGINLH — CDR-1, 24–34

TLQQEPDGTIKRLIY — Framework #2, 35–49

ATSSLGS — CDR-2, 50–56

GVPKRFSGSRSGSDYSLTISSLES^{GDFVAYYC} — Framework #3, 57–88

LQYASSPYT — CDR-3, 89–97

FGGGTKLEIK — Framework #4, 98–107

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Figure 3B

QAYLQQSGAELVRSGASVKMSCKASGYTLT — Framework #1, 1–30

SYNMH — CDR-1, 31–35

WVKQTPGQGLEWIG — Framework #2, 36–49

NIFPGNGDTYYNQKFKG — CDR-2, 50–66

KASLTADTSSSTAYMQISSLTSEDSAVYFCAR — Framework #3, 67–98

GNWEGALDY — CDR-3, 99–107

WGQGTSVTVSS — Framework #4, 108–118

DRAFT: 05/20/2010

Figure 4A

>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.

```

67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
127 CTCACTTGTGGCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCA 186
187 GATGGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAA 246
247 AGGTTCACTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCT 306
307 GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGAGGG 366
367 GGGACCAAGCTGAAATAAAA 387

```

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody light chain mRNA.

```

1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACTTGTGGCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAA 180
181 AGGTTCACTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGAGGG 300
301 GGGACCAAGCTGAAATAAAA 321

```

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.

```

313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
373 CTCACTTGTGGCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCA 432
433 GATGGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAA 492
493 AGGTTCACTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCT 552
553 GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTGGTGG 612
613 GGCACCAAGCTGAAATCAA 633

```

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).

```

314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
374 CTCACTTGTGGCCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCA 433
434 GATGGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAA 493
494 AGGTTCACTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCT 553
554 GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTGGTGG 613
614 GGCACCAAGCTGAAATCAA 634

```

>gb|I03643|I03643 Sequence 4 from patent US 4642334.

```

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
61 CTCACTTGTGGCCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCA 120
121 GATGGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAA 180
181 AGGTTCACTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTGGTGG 300
301 GGCACCAAGCTGAAATCAA 321

```

>gb|M59920|MUSIGKAA3 Mouse IG germline chain mRNA V-J region, partial cds.

```

1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
61 ACTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTAAACTGGCTTCAGCAGGAACCAAC 120
121 GGAACATTTAAACGCCGATCTACGCCACATCCAGTTAGATTCTGGTGTGCCAAAAGG 180
181 TTCAGTGGCAGTAGGTCTGGTCAGATTATTCTCACCATCAGCAGCCTTGAGTCTGAA 240
241 GATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTGGTGGAGGC 300
301 ACCAAGCTGAAATCAA 318

```

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>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H220-23.

1 TCTCCATCCTCCTTATCTGCCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGT 60
61 CAGGACATGGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGAACTATTAAACGC 120
121 CTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCCAAAAGGTTAGTGGCAGTAGG 180
181 TCTGGGTCAAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGACTAT 240
241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGAGGGGGACCAAGCTGNAATA 300
301 AAA 303

>emb|Z22118|MDIGKVBS M.domesticus IgK variable region.

1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTGGGAGAAAGAGTCAGT 60
61 CTCACTTGTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120
121 GATGGAACATTAAACGCCGATCTACAGCACATCCACTTAAATTCTGGTGTCCCCAAA 180
181 AGGTTCAAGTGGCAGTAGGTCTGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
241 GAAGATTTCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGAGGG 300
301 GGGACCAAACGGAAATAAAA 321

>gb|M64168|MUSIGKAFT Mouse Ig active kappa-chain mRNA V-region.

4 TCTCCATCCTCCTTATCTGCCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGT 63
64 CAGGACATGGTAATAGCTTAAACTGGCTTCAGCAGGAACCAGATGAACTATTAAACGC 123
124 CTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCCAAAAGGTTAGTGGCAGTAGG 183
184 TCTGGGTCAAGATTATTCTCTCACCATCAGCAGCCTTGAACTCTGAAGATTTGTAGTCTAT 243
244 TACTGTCTACAATATGCTAGTTACGTACACGTTGGAGGGGGACCAAGTTGAACTA 303
304 AAA 306

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain(partial)
Cloop 1

42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTGGGAGAAAGAGTCAGT 101
102 CTCACTTGTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
162 GATGGAACATTAAACGCCGATCTACGCCGATCCACTTAAAGATTCTGGTGTCCCCAAA 221
222 AGGTTCAAGTGGCAGTAGGTCTGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
282 GAAGATTTCAGACTATTACTGTCTACAATATCTTAGTTACGTACACGTTGGAGGGGGACCAAGTTGAACTA 341
342 GGGACCAAAGCTGGAGCTGAAA 362

Figure 4B

>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATNTACAGCAGTCTGGGCTGAGCTGGTGAGGCCTGGGCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGGTAAAGCAGACA 120
121 CCTAGACAGGGCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357 .

```

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA antibody heavy chain mRNA.

```

1 CAGGCTTATGTACAGCAGTCTGGGCTGAGCTGGTGAGGCCTGGGCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACAGATTACAGTTACAATATGCACTGGTAAAGCAGACA 120
121 CGTAGACAGGGCTGGAATGGATTGGAGCAATTATCCAGGAAATGGTATACTTCCTAT 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGAGA 298
299 GGGGTAACACTACGTAGGACATATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCC 357
358 TCA 360

```

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region.

```

1 CAGGCTTATCTACAGCAGTCTGGGCTGAGCTGGTAAGGCCTGGGCTCAGTGAAGATG 60
61 TCCTGCAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGGTAAAGCAGACA 120
121 CCTAGACAGGGCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTATACTTCCTAC 180
181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
241 ATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAT 300
301 TACTCCGGTAGTATAGACTACTGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

```

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.

```

96 CAGGCTTATCTACAGCAGTCTGGGCTGAGCTGGTGAGGCCTGGGCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGGTAAAGCAGACA 215
216 CCTAGACAGGGCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394.

```

96 CAGGCTTATCTACAGCAGTCTGGGCTGAGCTGGTGAGGCCTGGGCTCAGTGAAGATG 155
156 TCCTGCAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGGTAAAGCAGACA 215
216 CCTAGACAGGGCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTATACTTCCTAC 275
276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335
336 ATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGTG 392
393 ----- 427
428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 457

```

Figure 5A

>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.

```

2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGCTTCAGTGAAGATAT 61
62 CCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTGAAGCAGAAC 121
122 CTGGGCAGGGCCTTGAGTGGAGAGATTATCCTGGAAGTGGTAATACTTACTACA 181
182 ATGAGAAGTTCAAGGGYAAAGGCCACTGACTGCAGACAAATCCTCCAGCACAGCCTAC 241
242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTCTGTGCAAGACGTTACT 301
302 ----- 314
315 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTCAGCTCCAGCAGTCTGGGCTGAGCTGGCAAGACCTGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTACTAGCTACTGGATGCAGTGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGCTATTTATCCTGGAGATGGTGTAACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAG 295
296 ----- 314
315 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

```

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTCAGCTCCAGCAGTCTGGGCTGAGCTGGCAAGACCTGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTACTAGCTACTGGATGCAGTGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGCTATTTATCCTGGAGATGGTGTAACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA 294
295 ----- 317
318 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.

```

1 CAGGTTCAGCTCCAGCAGTCTGGGCTGAGCTGGCAAGACCTGGGCTTCAGTGAAGTTG 60
61 TCCTGCAAGGCTTCTGGCTACACCTTACTAGCTACTGGATGCAGTGGTAAAACAGAGG 120
121 CCTGGACAGGGTCTGGAATGGATTGGGCTATTTATCCTGGAGATGGTGTAACTAGGTAC 180
181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAAATCCTCCAGCACAGCCTAC 240
241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA 294
295 ----- 311
312 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J) anti-DNA autoantibody.

```

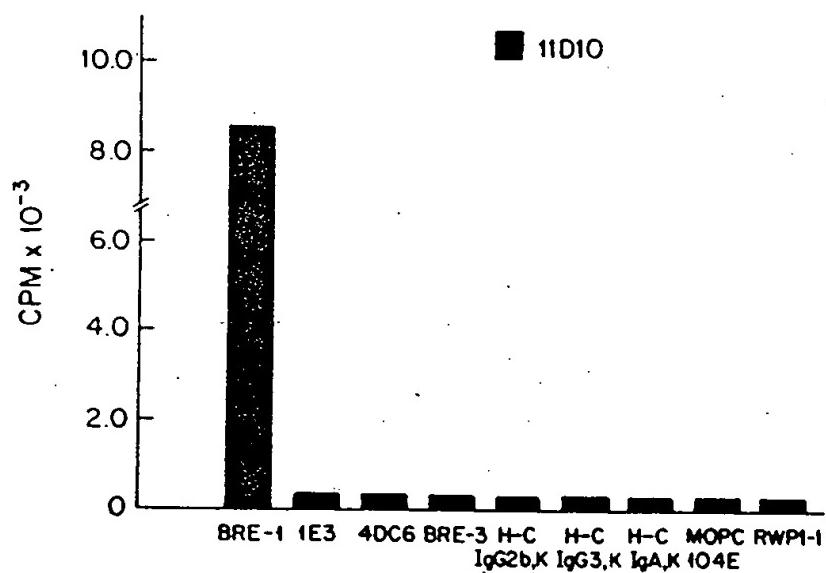
106 CAGGTCCAAGTGCAGCAGCCTGGTGTGAGCTTGTGAAGCCTGGGCTCAGTGAAGCTG 165
166 TCCTGCAAGGCTTCTGGCTACACCTTCAACAGCTACTGGATAAAACTGGGTGAAGCAGAGG 225
226 CCTGGACAAGGCCTTGAGTGGATTGAAATATTTATCCTGGTAGTGTAGTACTAACTAC 285
286 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 345
346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCAGTCTATTGTGCAAGACG 401
402 ----- 416
417 TGCTATGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462

```

Figure 5B

08/766350

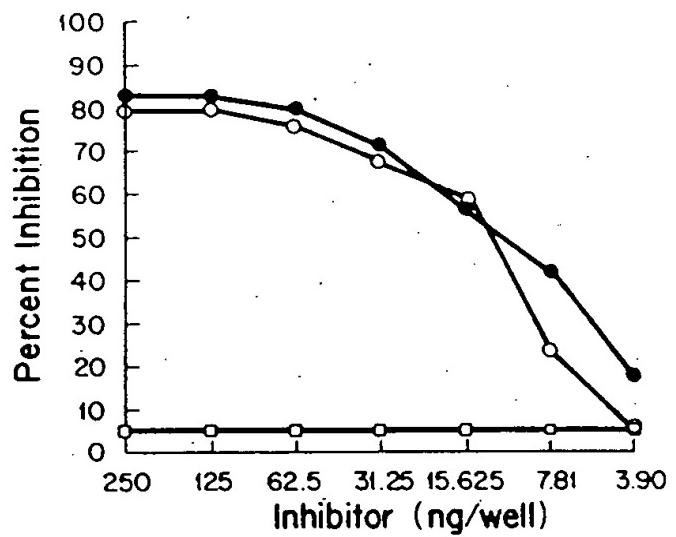
Figure 6



96350-121290

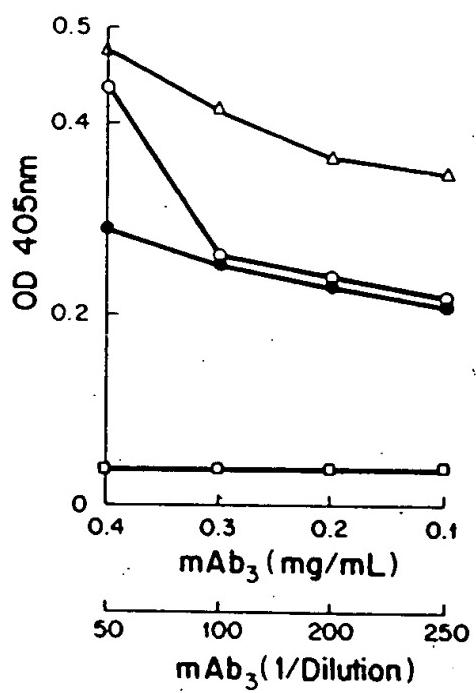
08/766350

Figure 7



08/766350

Figure 8

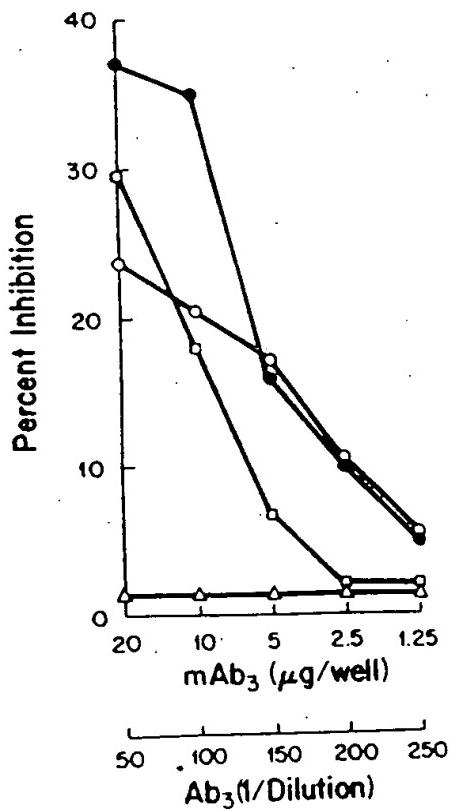


00000000000000000000000000000000

08/766350

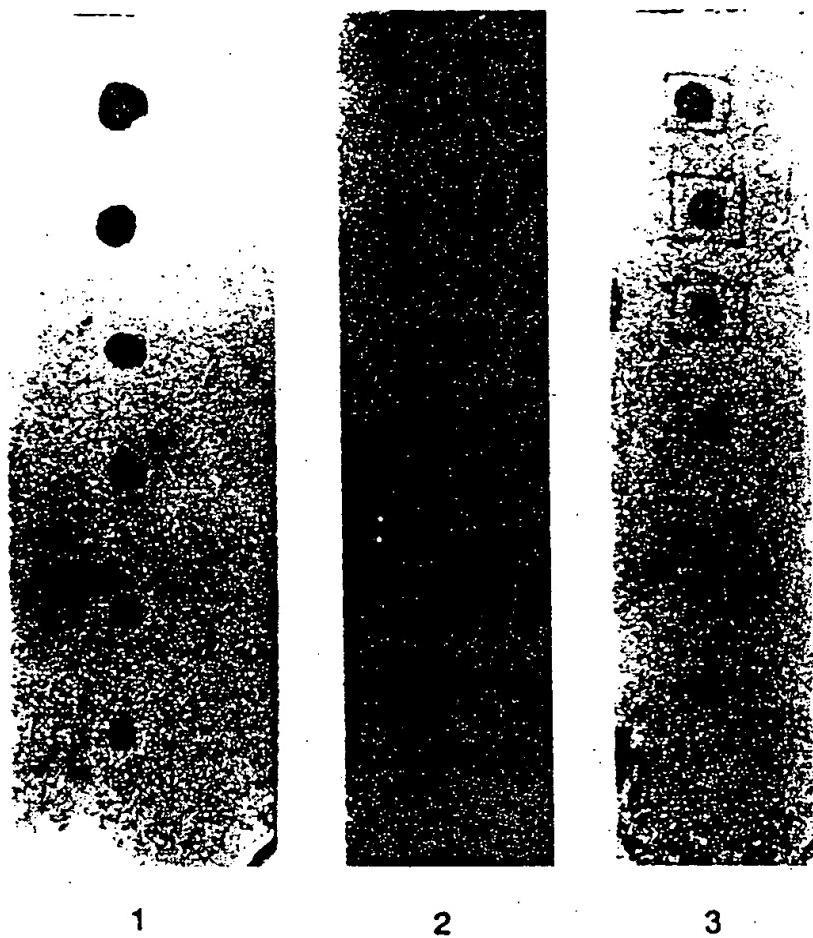
PIGEMENT "OSSEOUS"

Figure 9



08/766350

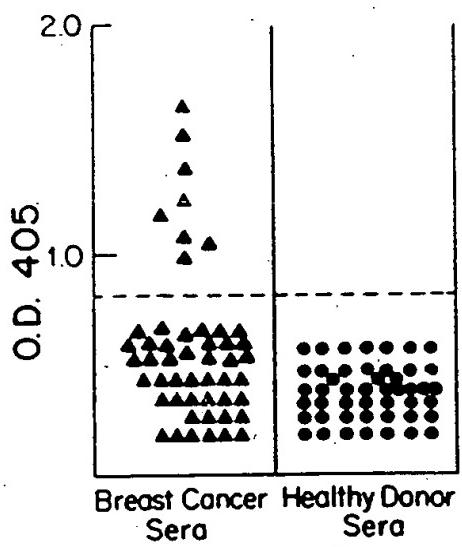
Figure 10



08/766350 - DATE 06/06/80

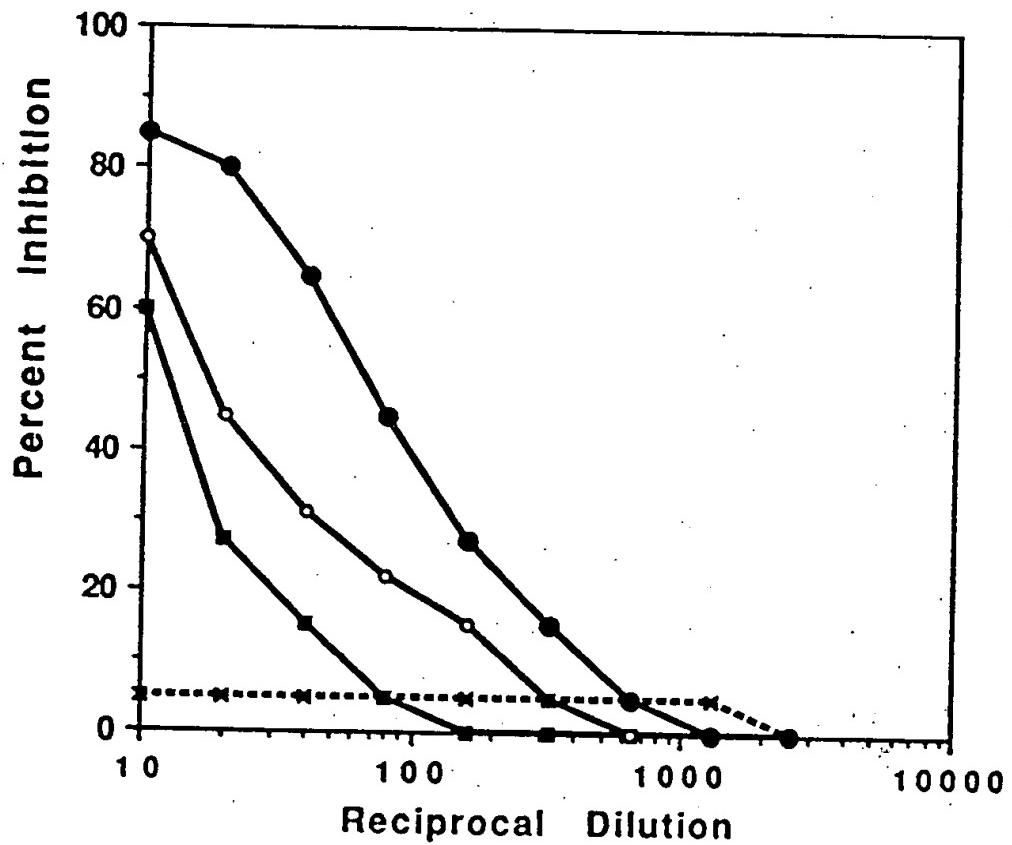
08/766350

Figure 11



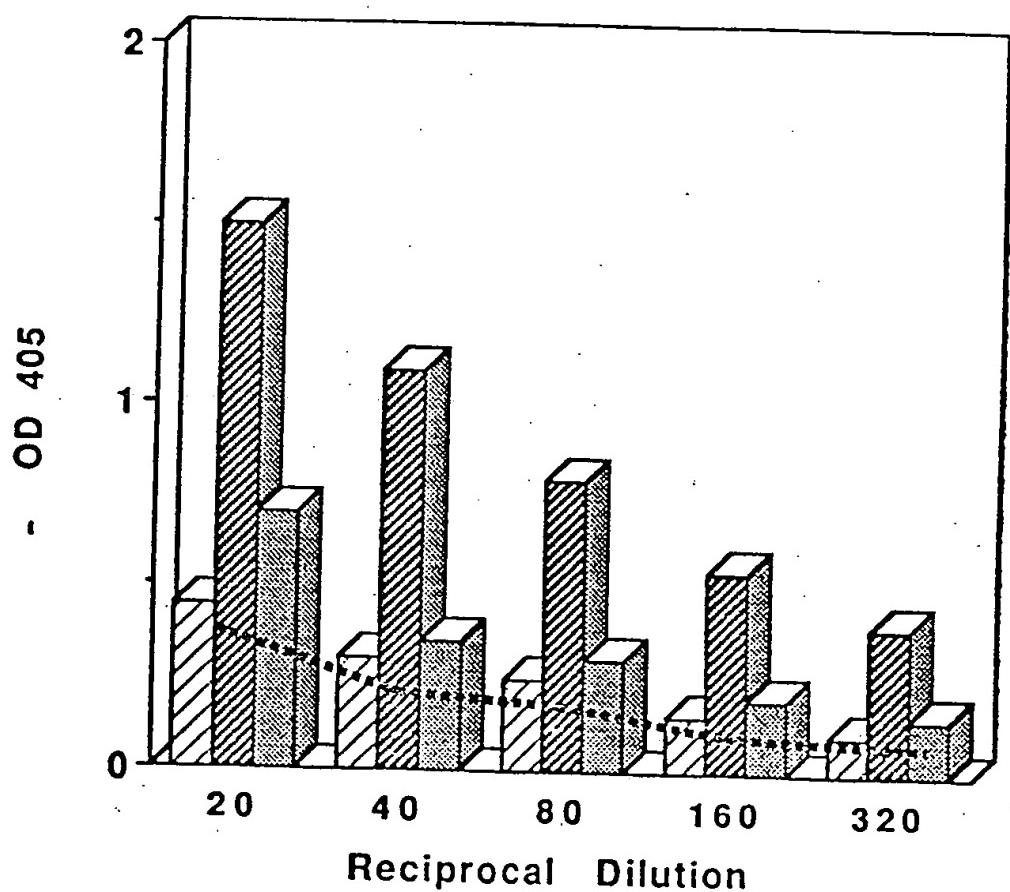
08/766350

Figure 12



08/766350

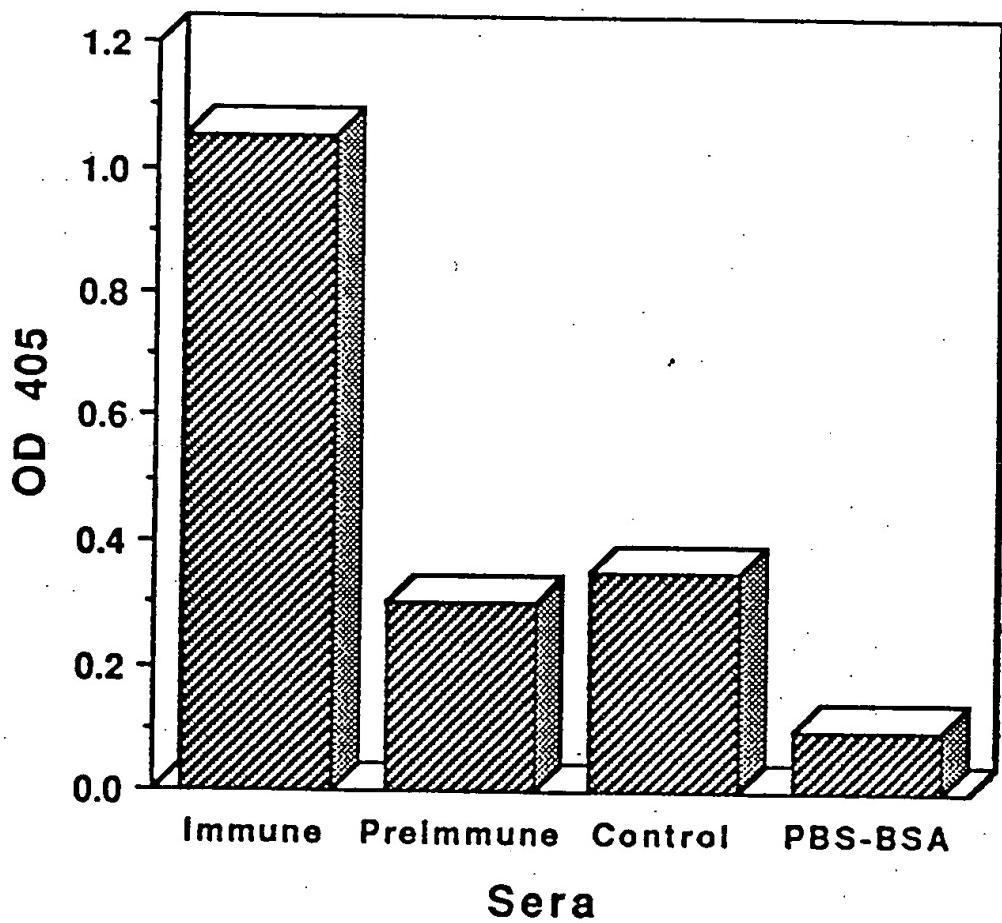
Figure 13



08/766350 121395

08/766350

Figure 14



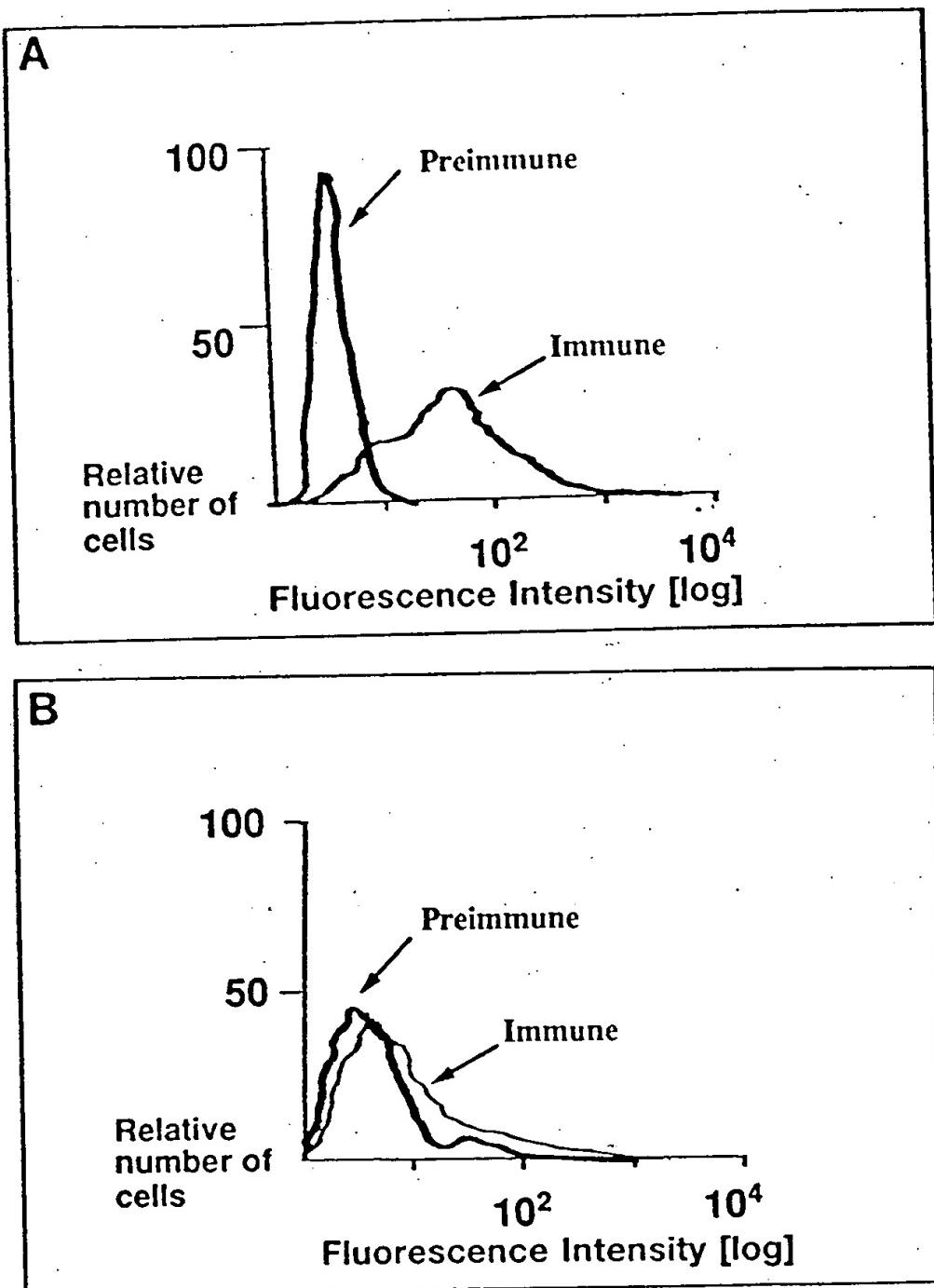
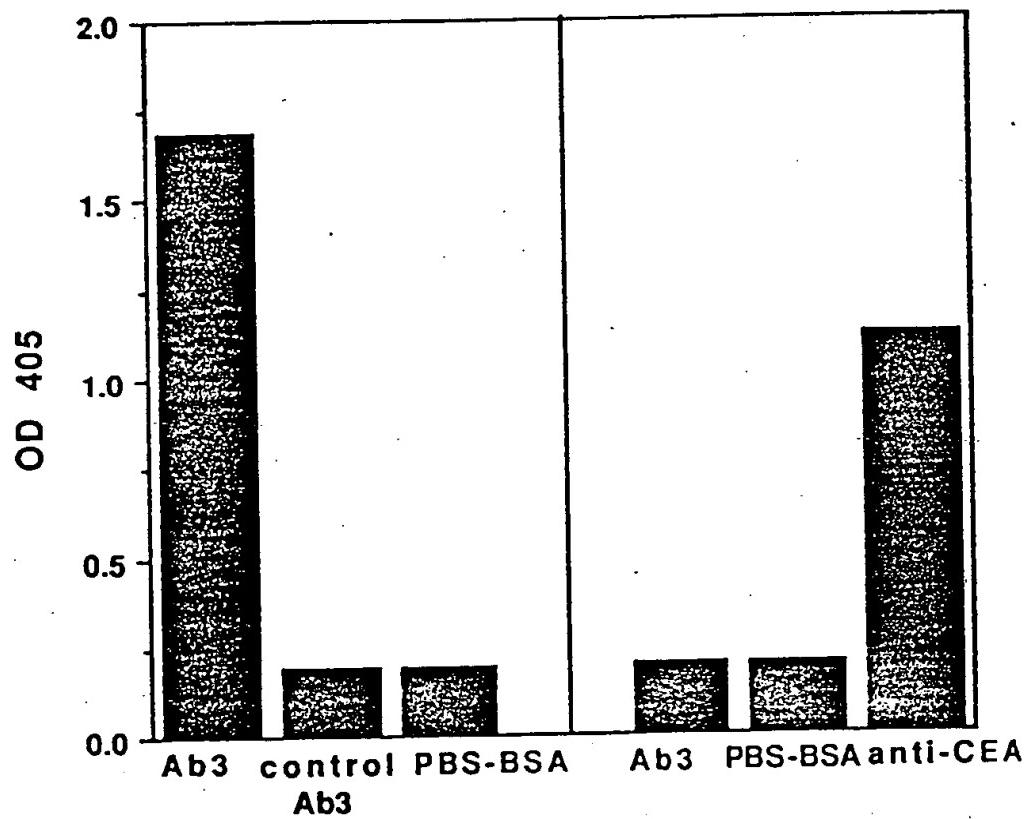


Figure 15

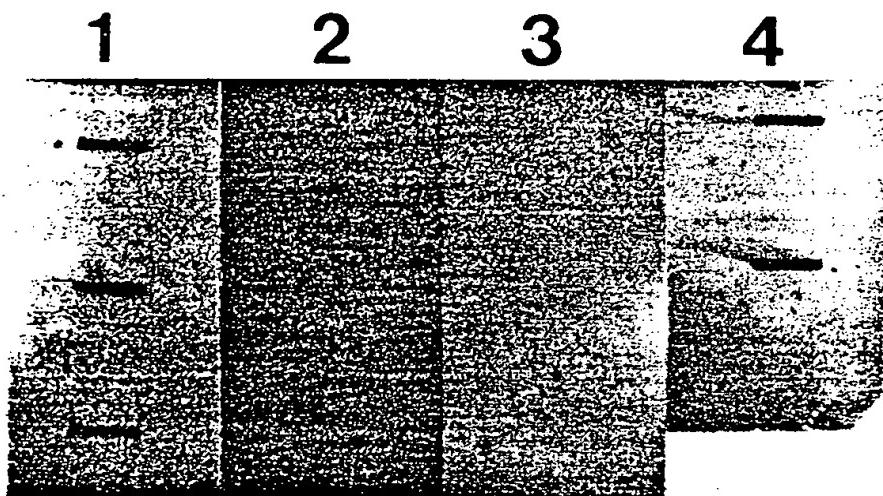
08/766350

Figure 16



08/766350

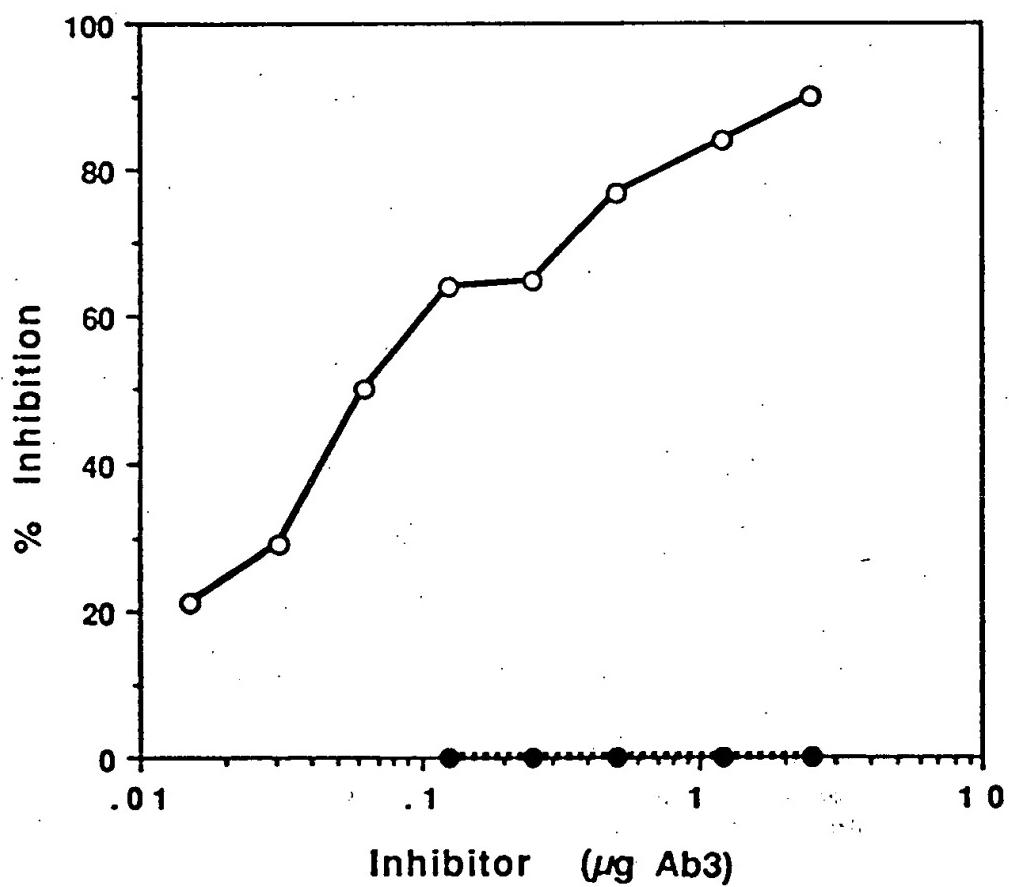
Figure 17



08/766350-121396

08/766350

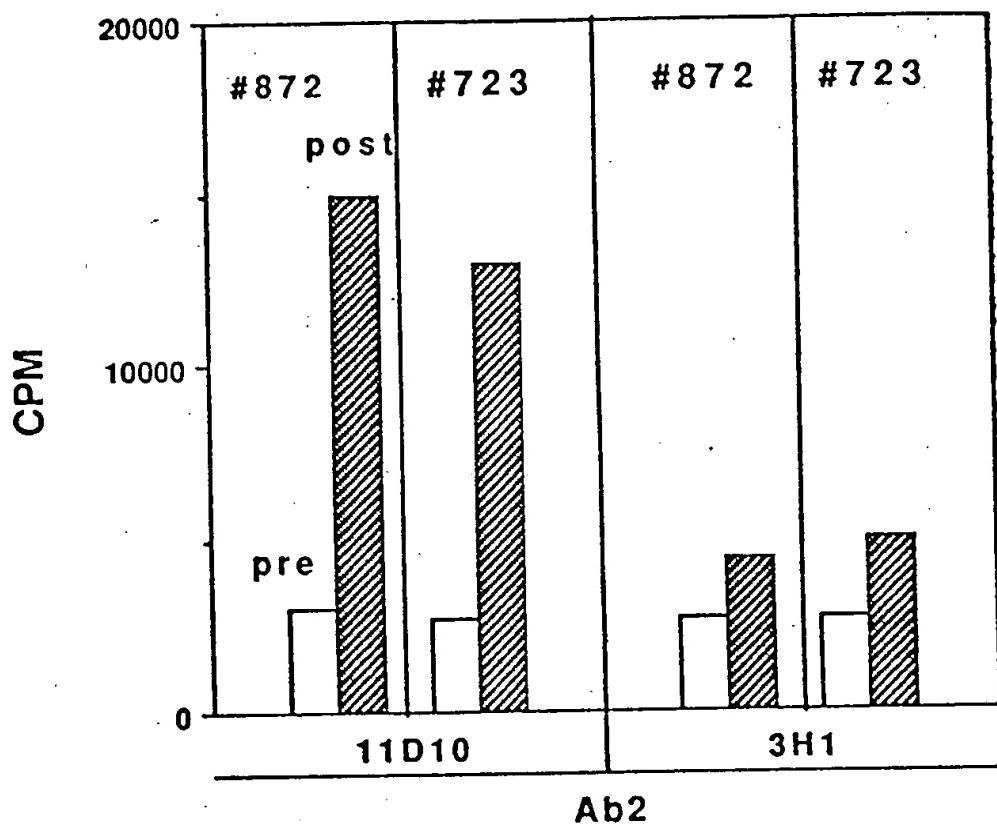
Figure 18



08/766350-121395

08/766350

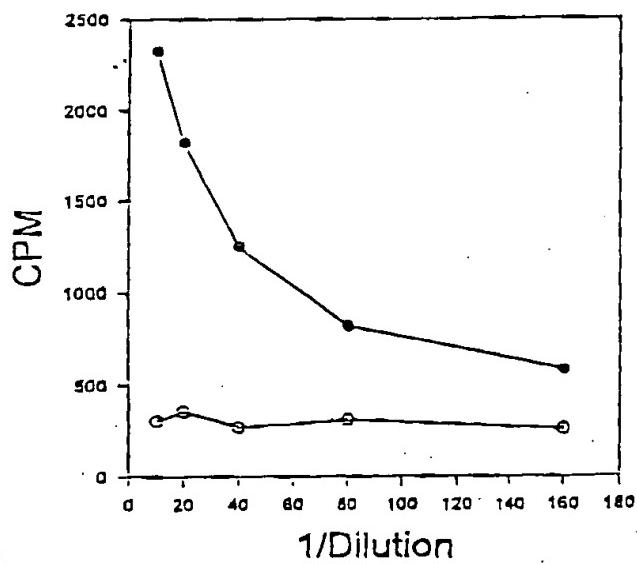
Figure 19



08/766350 - 121396

08/766350

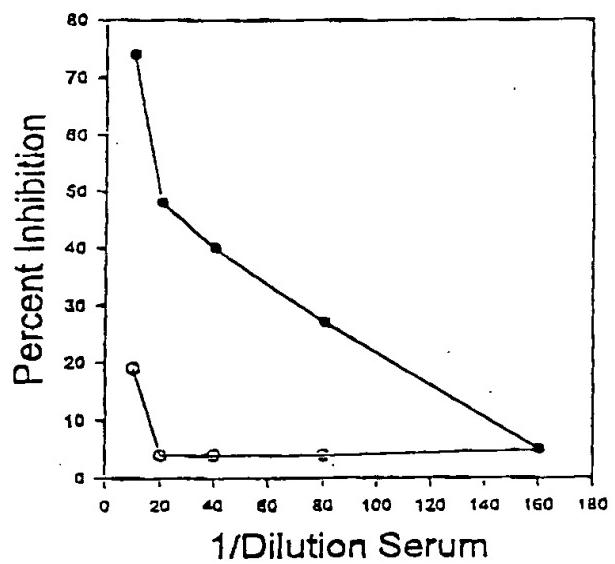
Figure 20



3637105299X810

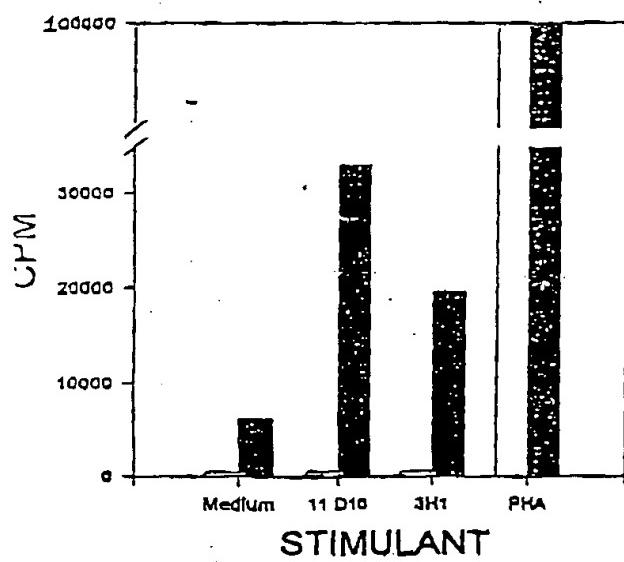
08/766350

Figure 21



08/766350

Figure 22



08/766350 - FIGURE 22

08/766350

Figure 23

Alignment of 11D10 CDRs with HMFG Tandem Repeat

Q G L E W I G N I F P G N G D T Y Y N O	V _H (near CDR 2)
: : : :	
R E S P	
G S T A P P A H G V T S A P D T R P A P	HMFG repeat (direct)
:	
D G T I K R L I Y A T S S L G S G V P L	V _L (near CDR 2)
P S E R P	
F A P R T D P A S T V G H A P P A T S G P A P	HMFG repeat (rev.)
: : : : : : : :	
H T L Q Q E P D G T I K R L I Y A T S S L G S	V _L (near CDR 2)
: : : :	
A Y Y C L O Y A S S P Y T F G G G T K L E I K	V _L (near CDR 3)

08/766350

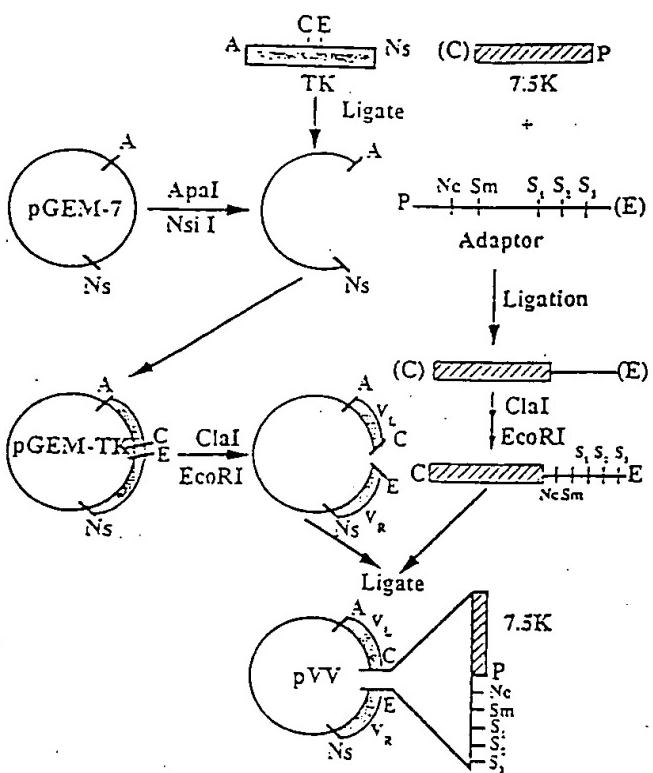


Figure 24

08/766350

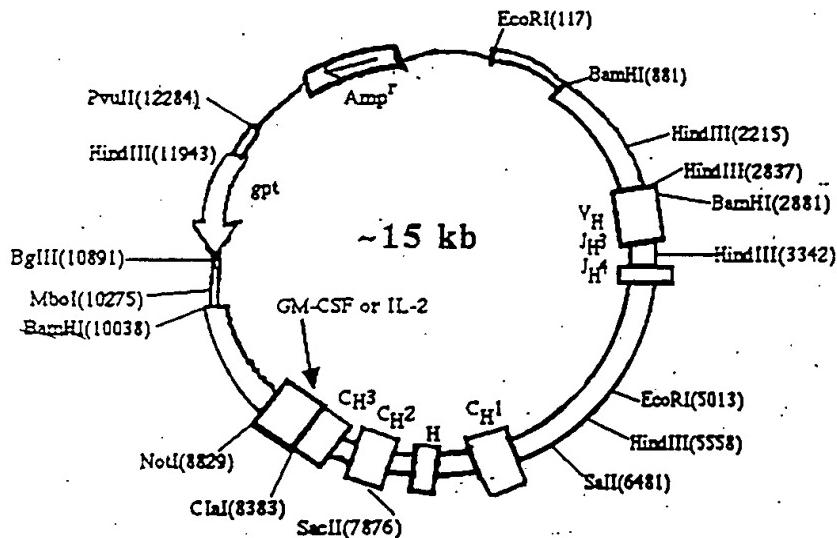


Figure 25A

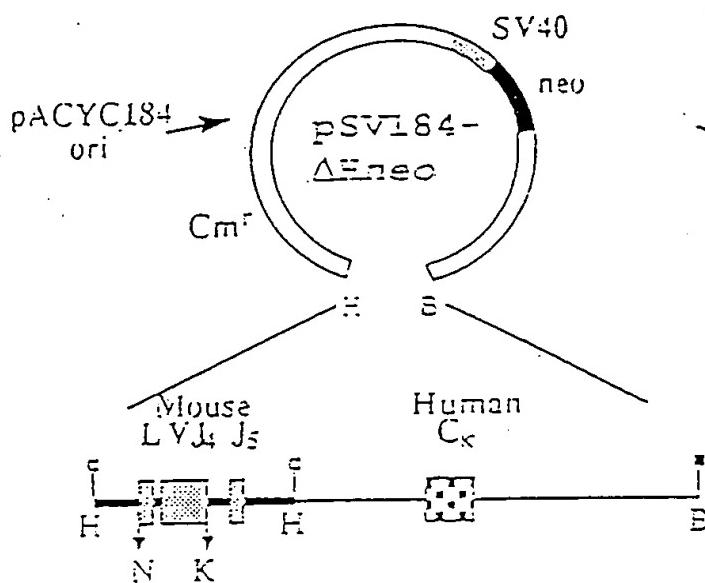


Figure 25B

08/766350

Figure 26(A)

11D10: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

1	23E.....SS.NW.....D....	82
2	23E.....SS.NW.....D....	82
3	23E.....SS.NW.....D....	82
4	23E.....P.....SS.NW.....D....	82
5	1E.....SS.NW.....D....	60
6	1E.....SS.NW.....D....	59
7	1E.....RS.NW.....D....	60
8	1E.....E.SGY.SW..K.....S.T.N....	60
9	1E.....SS.NW.....D....	54
10	1E.....E.SGY.SW..K.....A.T.D....	60
11	1	X.....E.....NS.NW.....D....	55
12	1E.....A.....E.GY.SW..K.....A.T.D....	60
13	14E.....E.SGY.SW..K.....A.T.D....	73
14	1	EL.....E.....E.SGY.SW..K.....A.T.D....	60
15	2	ELVL.....E.....E.NGY.GW..K.....A.T.H....	61

11D10: 61 RFSGSRSGSDYSLTISSLESEDVFAYYCLQYASSPYTFGGGTLEIK 107

1	83D.....	129
2	83D.....W.....	129
3	83D.....W.....	129
4	83D.....W.....	129
5	61D.....W.....	106
6	60D.....W.....	106
7	61D.....T.W.....	106
8	61AD.....	107
9	55D.....X..	107
10	60AD.....	106
11	56V.....YT.....L.	102
12	61G.....AD.....Y.W.....	106
13	74AD.....L.Y.L...A....L.	120
14	61AD.....Y.L...A....L.	107
15	62AD.....Y.R.....	108

Figure 26(B)

03766350-121396

11D10:	1	QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY	60
1	1P.S.....F.....R.....A.Y.....S.	60
2	20P.....F.....R.....A.Y.....S.	79
3	1	EVQ.....P...KP.....I.....F.D.Y.....K.....E.Y..S.N...	60
4	1	.IQ.....P....P....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
5	1	.VQ.....P...KP.....L.....F.D.TI.....S.....W.Y..S.N.K.	60
6	1	.VQ..E.....KP.....L.....F..W.....R.....K.N.S..R.N.	60
7	20	.VQ.....AKP.....F.A.W.....R.....Y.N.NT.Y.E.	79
8	1	EVQ.....KP.....L.....F..W.....R.....E.D.SDSY...	60
9	1	.VQ....E..A.P.....F.R.W.....R..A.....A.Y...S..N.	60
10	1	.VQ.....P.T..I.....F.N.WLG.....R..H.....D.Y..G.Y.N.	60
11	20	.VQ.....AKP.....F..R.....R.....Y.N.ST.Y.E.	79
12	1	.VQ.....AKP.....F..W.....R.....Y.N.ST.Y.E.	60
13	1	.IQ.....P....P....I.....F.D.YI.....R..E.....W.Y..S.N.K.	60
14	1	.VQ.....P.T.....A..F.N.WIG.....R..H.....D.Y..G.Y.N.	60
15	1	EVQ.....TV.A.P.....F..W.....R.....A.Y...S..R.	60
11D10:	61	NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG=NWEG=ALDYWGQGTSVTVSS	118
1	61T..V.K.....L.....=DYS.=SI.....TL....	118
2	80T..V.K.....L.....xxxxxxxxxx=xx.V..T..T....	140
3	61	.E.....K.....L.....xxxxxx==.M.....	120
4	61	.E.....T..V.....L.....==xxx==.M.....	117
5	61	.D.....TM..K.....L.....=VAR.S=.M.....	119
6	61	.E...S..T..V.K.....L.....Y...xxxxxxxxx.....T....	123
7	80	..N..D..T..K.....L.....Y.T.xxx.Y..==.M.....	139
8	61T..V.K.....F.....Y...xxxxxxxx=xM.....	120
9	61K..V..A..EL..A.....Y..S=RYS.=SM.....	119
10	61	.E.....T.....L.....P=HYY.=SG.....TL....	118
11	80D..T..K.....L..F.....Y...==x.=VF.....TL....	135
12	61D..T..K.....L.....L.Y..W=VYYY==.M.....	118
13	61	.E.....T..V.....L.....==xxx==.M.....	117
14	61	.E.....T.....L.....I.Y..P=FYFY==.M.....C....	118
15	61K..V..A..EL..N.....Y.T..=GLFT==.M.....	115

Figure 26(C)***Light Chain***

	*****	*****
VL consensus:	1 DIQMTQSPSSLASLGERVSLTCRASQD I GSSLNLQQEPDGTIKRLIYATSSLDSGVPK	60
11D10:	1Q.....IN.HT.....G.....	60
HMFG fragments:	<u>GSTAPPAAHRVTSAPESRPPP</u> ppprsepastvrhappatsg	

	*****	*****
VL consensus:	61 RFSGSRSGSDYSLTISSLES I GDFVDDYCLQYASSPYTFGGGT I KLEIK	107
11D10:	61A.....	107
HMFG fragments:	ppprsepastvrhappatsg	

Heavy Chain

	*****	*****
VH consensus:	1 QVQLQQSGAELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNGDTNY	60
11D10:	1 .AY.....S.....L...N.....T.....N.F.....Y.	60
HMFG fragments:	<u>APDTRPPP</u>	

	*****	*****
VH consensus:	61 NQKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGxxxGAMDYWGQGTSVTVSS	118
11D10:	61S.....I.....NWE..L.....	118

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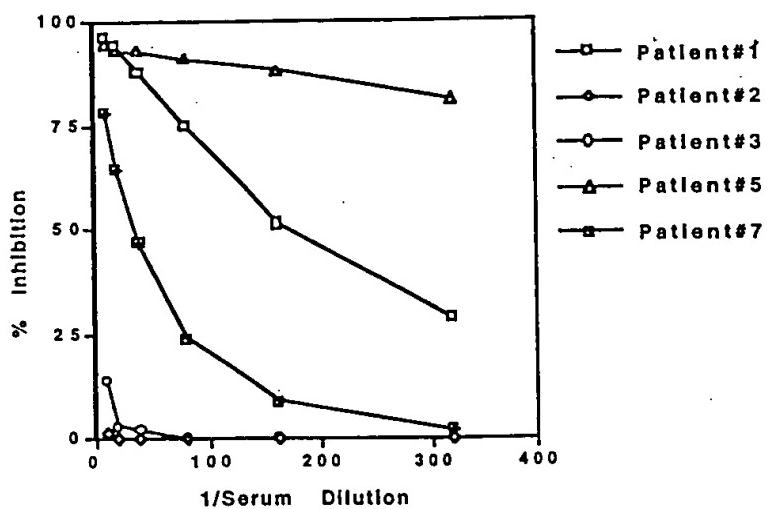


Figure 27A

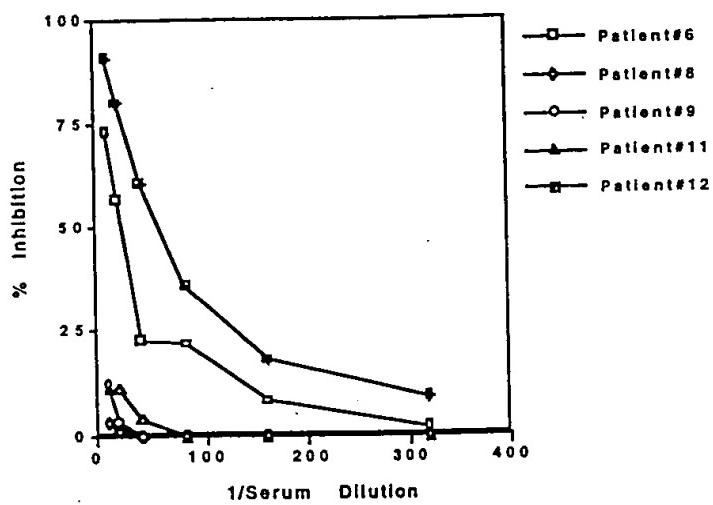


Figure 27B

08/766350

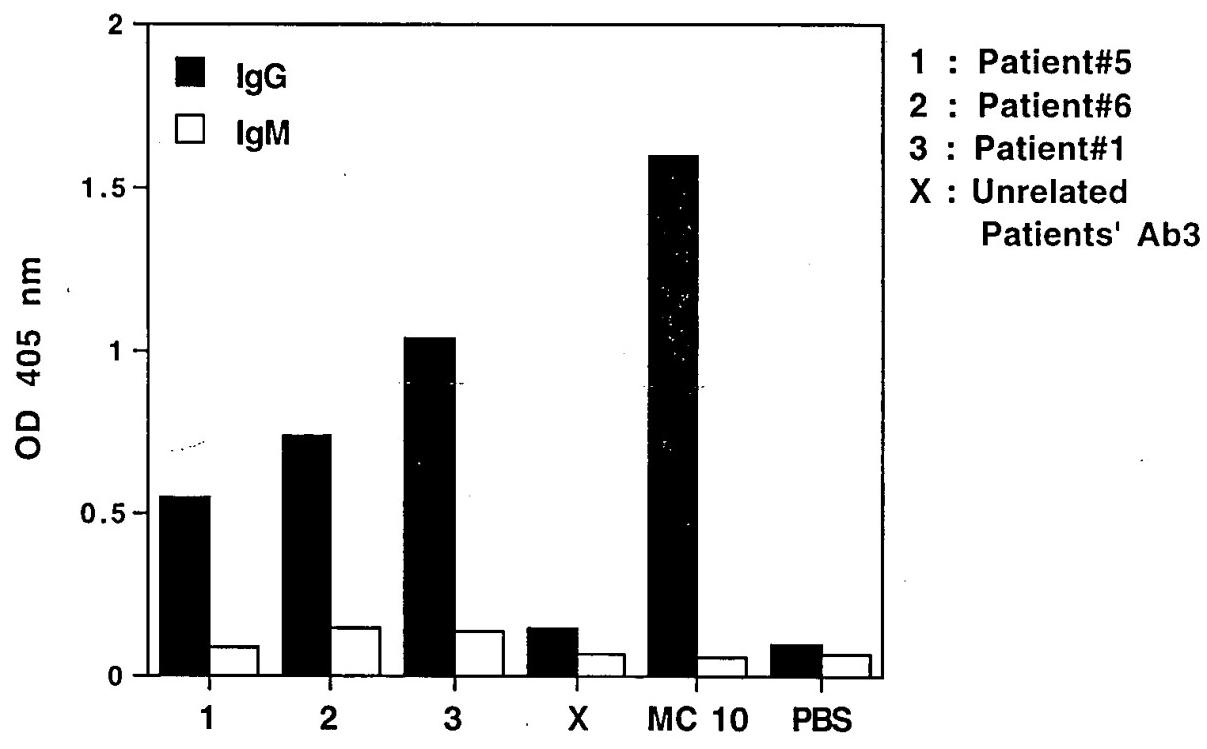


Figure 28

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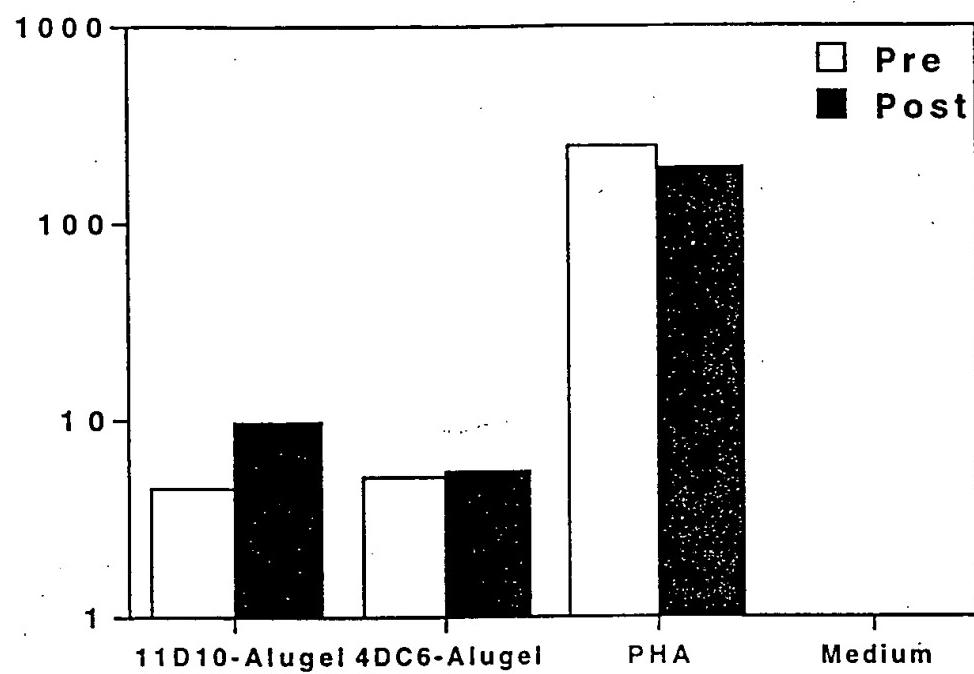


Figure 29 A

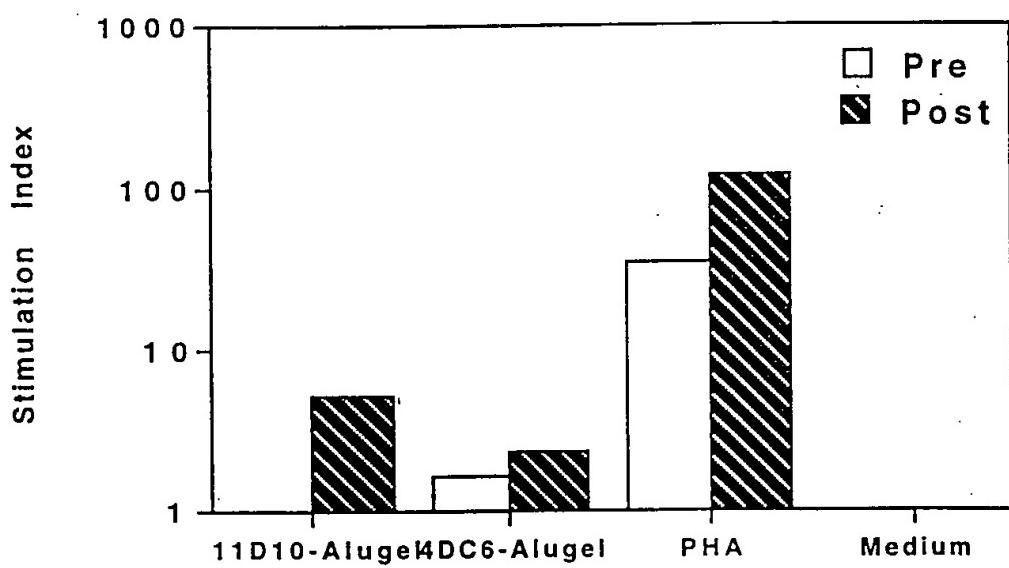


Figure 29B